Listing of Claims:

- 1-9: (Cancelled)
- 10. (Original) A method of determining the effect of a drug lead on the activity of a drug-metabolizing enzyme comprising:
- (a) providing a drug lead that shifts the thermal unfolding curve of a receptor regulating cytochrome P450 expression; and
- (b) screening the drug lead for its ability to further shift the thermal unfolding curve of the receptor in the presence of one or more co-regulators; wherein a further shift in the thermal unfolding curve of the receptor in the presence of the drug lead and a co-regulator of said one or more co-regulators indicates whether the drug lead increases the activity of a drug-metabolizing enzyme.
- 11. (Original) The method of claim 10, wherein providing a drug lead that shifts the thermal unfolding curve of the receptor comprises screening one or more of a multiplicity of different molecules for their ability to shift the thermal unfolding curve of the receptor.
- 12. (Original) The method of claim 11, wherein said screening of one or more of a multiplicity of different molecules comprises:
- (a) contacting said receptor regulating cytochrome P450 and one or more molecules in each of a multiplicity of containers;
- (b) heating said receptor in each of said multiplicity of containers to cause said receptor to unfold;
- (c) measuring in each of said containers a physical change associated with the thermal unfolding of said receptor;
 - (d) generating a thermal unfolding curve for said receptor for each of said containers;

- (e) comparing each of said thermal unfolding curves in step (d) to:
 - (i) each of the other thermal unfolding curves; and/or
- (ii) the thermal unfolding curve for said target molecule in the absence of any of said multiplicity of molecules; and
- (f) determining whether any of said multiplicity of molecules shifts the thermal unfolding curve of said receptor.
- 13. (Presently Amended) The method of claim 10 or claim 12, wherein said screening step further comprises:
- (a) contacting said drug lead and said receptor regulating cytochrome P450 expression with one or more of said co-regulators in each of a multiplicity of containers;
- (b) heating said receptor in each of said multiplicity of containers to cause said receptor to unfold;
- (c) measuring in each of said containers a physical change associated with the thermal unfolding of said receptor;
 - (d) generating a thermal unfolding curve for said receptor for each of said containers;
 - (e) comparing each of said thermal unfolding curves in step (d) to:
 - (i) each of the other thermal unfolding curves; and/or
 - (ii) the thermal unfolding curve for said receptor in the absence of (1) said drug lead and/or (2) said co-regulators; and
 - (f) determining whether said drug lead further shifts the thermal unfolding curve of said receptor.

- 14. (Original) The method of claim 10 wherein the one or more co-regulators includes a co-activator and/or co-repressor.
- 15. (Original) The method according to claim 10, wherein the molecule further modifies the stability of the receptor in the presence of a co-activator, thereby identifying the ligand as an agonist of the receptor when in the presence of the co-activator.
 - 16. (Original) The method according to claim 15, wherein the agonist is a partial agonist.
- 17. (Original) The method according to claim 10, wherein the molecule further modifies the stability of the receptor in the presence of a co-repressor, thereby identifying the ligand as a non-agonist of the receptor when in the presence of the co-activator.
 - 18. (Original) The method according to claim 17, wherein the non-agonist is a partial agonist.
 - 19-21. (Cancelled)
- 22. (Original) A method of identifying an agonist of xenobiotic metabolism comprising screening a molecule for its ability to shift the thermal unfolding curve of a receptor regulating cytochrome P450 expression and to further shift the thermal unfolding curve of said receptor when in the presence of one or more co-activators; wherein a molecule that shifts the thermal unfolding curve of said receptor when in the presence of a co-activator is identified as an agonist of xenobiotic metabolism.
 - 23. (Original) The method of claim 22, wherein said screening step further comprises:
- (a) contacting said molecule and said receptor regulating cytochrome P450 expression with one or more of said co-activators in each of a multiplicity of containers;
- (b) heating said receptor in each of said multiplicity of containers to cause said receptor to unfold;
- (c) measuring in each of said containers a physical change associated with the thermal unfolding of said receptor;

- (d) generating a thermal unfolding curve for said receptor for each of said containers;
- (e) comparing each of said thermal unfolding curves in step (d) to:
 - (i) each of the other thermal unfolding curves; and/or
- (ii) the thermal unfolding curve for said receptor in the absence of (1) said molecule and/or (2) said co-activators; and
- (f) determining whether said molecule further modifies the stability of said receptor, wherein a further modification in stability is indicated by a further change in said unfolding curve.
- 24. (Original) A method according to claim 22, wherein the agonist is a partial agonist.
- 25-26. (Cancelled)
- 27. (Original) A method of identifying a non-agonist of xenobiotic metabolism comprising screening a molecule for its ability to shift the thermal unfolding curve of a receptor regulating cytochrome P450 expression; wherein a molecule that does not shift the thermal unfolding curve of said receptor is identified as a non-agonist of xenobiotic metabolism.
 - 28. (Original) The method of claim 27, wherein said screening step comprises:
- (a) contacting said receptor regulating cytochrome P450 and one or more molecules in each of a multiplicity of containers;
- (b) heating said receptor in each of said multiplicity of containers to cause said receptor to unfold;
- (c) measuring in each of said containers a physical change associated with the thermal unfolding of said receptor;
 - (d) generating a thermal unfolding curve for said receptor for each of said containers;
 - (e) comparing each of said thermal unfolding curves in step (d) to:

- (i) each of the other thermal unfolding curves; and/or
- (ii) the thermal unfolding curve for said target molecule in the absence of any of said multiplicity of molecules; and
- (f) determining whether said molecule modifies the thermal unfolding curve of said receptor.
- 29-60. (Cancelled)
- 61. (Currently Amended) A method according to any of claims 1-60 claim 10, wherein the co-regulator is a co- activator and/or a co-repressor.
- 62. (Currently Amended) A method according to any of claims 1-60 claim 10, wherein an agonist for a co-regulator dependent receptor is a strong inducer.
- 63. (Original) A method according to claim 62, wherein the strong inducer is $11-\alpha$ -hydroxyprogesterone.
- 64. (Currently Amended) A method according to any of claims 1.60 claim 10, wherein the strong inducer has a binding affinity of less than about 5μ M and a statistical probability of agonist state of about 0.8 to about 1.0.
- 65. (Currently Amended) A method according to any of claims 1-60 claim 10, wherein a partial agonist of a co-regulator dependent receptor is a weak inducer.
- 66. (Original) A method according to claim 65, wherein the weak inducer has a binding affinity of less than about 5 μ M and a statistical probability of agonist state of about 0.4 to about 0.8.
- 67. (Original) a method according to claim 65, wherein the weak inducer has a binding affinity of at least about 5 μ M and a statistical probability of agonist state of about 0.4 to about 1.0.
- 68. (Currently Amended) A method according to any of claims 1-60 claim 10, wherein an antagonist of a co-regulator dependent receptor is a non-inducer.

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- 69. (Original) A method according to claim 68, wherein the non-inducer has a binding affinity of less than about 5 μ M and a statistical probability of agonist state of less than about 0.4.
- 70. (Original) A method according to claim 65, wherein the non-inducer has a binding affinity of at least about 5 μ M and a statistical probability of agonist state of less than about 0.4.